

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:48:33 ; Search time 133.181 Seconds  
(without alignments)  
699.779 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTMGVPTQVLGILLMLTD.....CQVTHEGSTVKTVAPECS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1243	100.0	238	16 US-10-756-125-4
2	1089	87.6	235	9 US-09-747-669-6
3	1089	87.6	235	14 US-10-290-703-6
4	1070.5	86.1	236	9 US-09-758-173-10
5	1070.5	86.1	236	9 US-09-948-4298-10
6	1070.5	86.1	236	13 US-10-124-905-10
7	1070.5	86.1	236	14 US-10-124-807-10
8	1070.5	86.1	236	14 US-10-291-532-10
9	1070.5	86.1	236	18 US-10-986-780-10
10	1067	85.8	233	16 US-10-723-860-27
11	1067	85.8	268	15 US-10-363-616-332

12	1025	82.5	214	17	US-10-887-231-19	Sequence 19, Appl
13	1020	82.1	214	17	US-10-887-228A-2	Sequence 2, Appl1
14	1020	82.1	214	17	US-10-887-231-6	Sequence 6, Appl1
15	1020	82.1	214	17	US-10-887-231-17	Sequence 17, Appl
16	1011	81.3	214	16	US-10-128-520-107	Sequence 107, Appl
17	1009	81.2	214	17	US-10-887-231-37	Sequence 37, Appl
18	1007.5	81.1	213	16	US-10-128-520-112	Sequence 112, Appl
19	1007	81.0	214	16	US-10-128-520-104	Sequence 104, App
20	1004.5	80.8	213	16	US-10-128-520-105	Sequence 105, App
21	981.5	79.0	234	14	US-10-194-801C-4	Sequence 4, App
22	970	78.0	221	13	US-10-001-857-202	Sequence 202, App
23	963.5	77.5	242	14	US-10-225-108A-14	Sequence 14, Appl
24	963.5	77.5	242	15	US-10-461-148-7	Sequence 7, Appl1
25	939.5	75.6	234	9	US-09-758-173-2	Sequence 2, Appl1
26	939.5	75.6	234	9	US-09-948-4298-2	Sequence 2, Appl1
27	939.5	75.6	234	13	US-10-124-905-2	Sequence 2, Appl1
28	939.5	75.6	234	14	US-10-124-807-2	Sequence 2, Appl1
29	939.5	75.6	234	14	US-10-291-532-2	Sequence 2, Appl1
30	939.5	75.6	234	18	US-10-986-780-2	Sequence 2, Appl1
31	935	75.2	216	17	US-10-887-231-31	Sequence 31, Appl
32	934	75.1	216	17	US-10-887-231-23	Sequence 23, Appl
33	932	75.0	216	17	US-10-887-231-25	Sequence 25, Appl
34	925	74.4	216	17	US-10-887-228A-10	Sequence 10, Appl
35	925	74.3	216	17	US-10-887-231-10	Sequence 10, Appl
36	923	74.3	216	17	US-10-887-231-29	Sequence 29, Appl
37	923	74.3	216	17	US-10-887-231-33	Sequence 33, Appl
38	922.5	74.2	215	16	US-10-128-520-133	Sequence 133, App
39	921	74.1	216	17	US-10-887-231-39	Sequence 39, Appl
40	919.5	74.0	235	16	US-10-663-244-154	Sequence 154, App
41	918	73.9	216	17	US-10-887-231-21	Sequence 21, Appl
42	916.5	73.7	215	16	US-10-128-520-116	Sequence 116, App
43	915.5	73.7	215	16	US-10-128-520-128	Sequence 128, App
44	915	73.6	216	16	US-10-128-520-119	Sequence 119, App
45	913.5	73.5	215	16	US-10-128-520-117	Sequence 117, App

ALIGNMENTS

RESULT 1  
US-10-756-125-4  
; Sequence 4, Application US/10756125  
; Publication No. US20040209244A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Dennis R.  
; APPLICANT: YEE, Sidney  
; TITLE OF INVENTION: ANTI-DENGUE VIRUS ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: 48503-00004  
; CURRENT APPLICATION NUMBER: US/10/756,125  
; PRIOR FILING DATE: 2004-01-12  
; PRIOR APPLICATION NUMBER: 60/443,924  
; PRIOR FILING DATE: 2003-01-31  
; NUMBER OF SEQ IDS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: light chain  
US-10-756-125-4

Query Match	100.0%	Score 1243;	DB 16;	Length 238;
Best Local Similarity	100.0%	Pred. No. 1.3e-84;		
Matches 238;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	KLTMGVPTQVLGILLMLTDARCSVLTQPPSASCTPGQRTVISCSTSNIGSTNVWY	60	
DB	1	KLTMGVPTQVLGILLMLTDARCSVLTQPPSASCTPGQRTVISCSTSNIGSTNVWY	60	
QY	61	QOLCTAPKLIYNDORPSGVDPFSGSKTSASLAIISGLOSDEADYCAAWDDSLN	120	

Result No.	Score	Query Match	Length	DB	ID	Description
1	1070.5	86.1	236	3	US-08-487-550-10	Sequence 10, Appl
2	1070.5	86.1	236	4	US-09-526-098-10	Sequence 10, Appl
3	1070.5	86.1	236	4	US-09-383-916-10	Sequence 10, Appl
4	1043.8	83.9	235	3	US-09-049-672A-12	Sequence 12, Appl
5	1010.8	81.3	236	3	US-09-049-672A-7	Sequence 7, Appl
6	986.5	79.4	234	4	US-09-372-425A-4	Sequence 4, Appl
7	940.5	75.7	235	2	US-08-378-939-12	Sequence 12, Appl
8	939.5	75.6	234	3	US-08-487-550-2	Sequence 2, Appl
9	939.5	75.6	234	4	US-09-526-098-2	Sequence 2, Appl
10	939.5	75.6	234	4	US-09-383-916-2	Sequence 2, Appl
11	935.5	75.3	235	3	US-09-049-672A-10	Sequence 10, Appl
12	874.5	70.4	233	3	US-08-523-894-6	Sequence 6, Appl
13	872	70.2	235	4	US-09-152-060-70	Sequence 70, Appl
14	869	69.9	235	4	US-09-152-060-88	Sequence 88, Appl
15	864.5	69.5	240	3	US-09-049-672A-11	Sequence 11, Appl
16	806.5	64.9	239	4	US-09-828-995B-26	Sequence 26, Appl
17	792	63.7	238	3	US-08-793-450-6	Sequence 6, Appl
18	701.5	56.4	216	4	US-09-291-299A-8	Sequence 8, Appl
19	679	54.6	217	4	US-09-291-299A-7	Sequence 7, Appl
20	653.5	52.6	216	4	US-09-291-299A-10	Sequence 10, Appl
21	643.5	51.8	216	4	US-09-291-299A-9	Sequence 9, Appl
22	631	50.8	229	3	US-08-751-359-22	Sequence 22, Appl
23	631	50.8	229	3	US-08-907-146-22	Sequence 22, Appl
24	576	46.3	200	6	5189147-10	Patent No. 5189147
25	576	46.3	200	6	5189147-10	Patent No. 5189147
26	567	45.6	109	2	US-08-761-277A-51	Sequence 51, Appl
27	552.5	44.4	111	4	US-09-424-840B-8	Sequence 8, Appl

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OM protein - protein search, using sw model  
Run on: August 24, 2005, 21:05:54 ; Search time 141.813 Seconds  
(without alignments)  
859.402 Million cell updates/sec  
Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTWGVPTQVLGLLLMLTD.....CQVTHEGSTVETKVTAPTECS 238  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1053.5	84.8	236	2	Q8NEJ1 homo sapien
2	1040	83.7	235	2	Q6GMW6 homo sapien
3	1018	81.9	236	2	Q6GMX4 homo sapien
4	1017	81.8	236	2	Q6GMV7 homo sapien
5	1012.5	81.5	235	2	Q6IN99 homo sapien
6	1004	80.8	237	2	Q6DHW4 homo sapien
7	1000	80.5	236	2	Q6GMX3 homo sapien
8	963	77.5	236	2	Q9GB61 homo sapien
9	961	77.3	236	2	Q6IPQ0 homo sapien
10	942.5	75.8	235	2	Q6PIK1 homo sapien
11	939	75.5	236	2	Q6PIQ7 homo sapien
12	933.5	75.1	235	2	Q6PUG0 homo sapien
13	901.5	72.5	233	2	Q6PUA3 homo sapien
14	894.5	72.0	234	2	Q8N355 homo sapien
15	892	71.8	236	2	Q6P5S3 homo sapien
16	886.5	71.3	234	2	Q6GMW3 homo sapien
17	877.5	70.6	235	2	Q6P2J1 homo sapien
18	875.5	70.4	233	2	Q8TBC9 homo sapien
19	868.5	69.9	234	2	Q6GMV8 homo sapien
20	865.5	69.6	233	2	Q8N5F4 homo sapien
21	857.5	69.0	234	2	Q7Z2U7 homo sapien
22	853.5	68.7	234	2	Q6NS95 homo sapien
23	851	68.5	233	2	Q6NS96 homo sapien
24	838.5	67.5	233	2	Q6GMW4 homo sapien
25	821	66.0	233	2	Q9G169 homo sapien
26	794	63.9	230	2	Q7Z2U3 homo sapien
27	791	63.6	240	2	Q8WUX3 homo sapien
28	722	58.1	235	2	Q9W111 homo sapien
29	591	47.5	233	2	Q6GNH3 xenopus lae
30	590	47.5	231	2	Q6GNB8 xenopus lae
31	555	44.7	139	2	Q6PJ17 homo sapien

32	551	44.3	106	2	Q8TCJ5	Q8tcj5 homo sapien
33	548	44.1	105	1	LAC HUMAN	P01842 homo sapien
34	525	42.2	213	1	ILLI HUMAN	P15814 homo sapien
35	510.5	41.1	235	2	Q6GMW0	Q6gmw0 homo sapien
36	510	41.0	236	2	Q6GMW1	Q6gmw1 homo sapien
37	506	40.7	236	2	Q6PIH7	Q6pih7 homo sapien
38	505	40.6	236	2	Q6PIH4	Q6pih4 homo sapien
39	503	40.5	234	2	Q7Z473	Q7z473 homo sapien
40	503	40.5	240	2	Q63ZL4	Q63zl4 xenopus lae
41	501	40.3	236	2	Q6PIL8	Q6pil8 homo sapien
42	497	40.0	236	2	Q6GMX0	Q6gmx0 homo sapien
43	494	39.7	236	2	Q6P5S8	Q6p5s8 homo sapien
44	494	39.7	236	2	Q6PII5	Q6pit5 homo sapien
45	493	39.7	236	2	Q6GMX8	Q6gmx8 homo sapien

ALIGNMENTS

RESULT 1

Q8NEJ1  
ID Q8NEJ1 PRELIMINARY; PRT; 236 AA.  
AC Q8NEJ1  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DB Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smailus D.E., Schnarch A., Schein J.R., Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC030984; AAH30984.1; -;  
DR HSSP; P01703; 7FAB.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:54:14 ; Search time 30.2124 Seconds  
(without alignments)  
757.952 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTMGVPTQVLGLLLMLTD.....CQVTHEGSTVKTVPTECS 238

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	88.5	233	2 S25752	Ig lambda chain -
2	1091	87.8	234	2 S25757	Ig lambda chain -
3	1068.5	86.0	216	2 A42193	Ig lambda chain (B
4	1067	85.8	233	2 S25744	Ig lambda chain -
5	1063	85.5	235	2 S25750	Ig lambda chain -
6	1053.5	84.8	235	2 S25754	Ig lambda chain -
7	1028.5	82.7	235	2 S05270	Ig lambda chain pr
8	1010.5	81.3	216	2 S03401	Ig lambda chain (K
9	1007.5	81.1	216	2 S25258	Ig lambda chain V
10	1004.5	80.8	232	2 S25742	Ig lambda chain -
11	998	80.3	213	2 S21066	Ig lambda chain V
12	984	79.2	236	2 S25746	Ig lambda chain -
13	969	78.0	217	2 JE0246	Ig lambda chain NI
14	942.5	75.8	235	2 S14675	Ig lambda chain -
15	921.5	74.1	208	2 B49444	Ig lambda chain (N
16	914.5	73.6	235	2 S25759	Ig lambda chain -
17	905.5	72.8	232	2 S25756	Ig lambda chain -
18	895.5	72.0	235	2 S25758	Ig lambda chain -
19	892.5	71.8	231	2 S25738	Ig lambda chain -
20	880.5	70.8	216	2 S69130	Ig lambda chain (D
21	879.5	70.8	233	2 S25751	Ig lambda chain -
22	875	70.4	233	2 S25747	Ig lambda chain -
23	868.5	69.9	216	2 JE0245	Ig lambda chain NI
24	864.5	69.5	233	2 S25741	Ig lambda chain -
25	860.5	69.2	231	2 S25753	Ig lambda chain -
26	857.5	69.0	235	2 S25748	Ig lambda chain -
27	843	67.8	232	2 S25749	Ig lambda chain -
28	841.5	67.7	213	2 JE0247	Ig lambda chain NI
29	841.5	67.7	226	2 S25745	Ig lambda chain -

ALIGNMENTS

RESULT 1

S25752  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25752  
R:Combiato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin 1  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25752  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-233 <COM>  
A:Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 1100; DB 2; Length 233;

Best Local Similarity 93.9%; Pred. No. 1.7e-61;

Matches 216; Conservative 3; Mismatches 7; Indels 4; Gaps 2;

QY	13	LLLLLWLTDA	---	COSVLTQPPSASGTGQRTV	ISCGSTSNIGSNVWYQOLPGTAPK	69
DB	4	LLLLLTHCAGSWAGSVLTQPPS	ASGTGQRTV	ISCGSSNIGSNVWYQOLPGTAPK	63	
QY	70	LLIYSNDQRP	SGVDP	PFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNG-LFGGGTK	128	
DB	64	LLIYNNQRP	SGVDP	PFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGVVGGGTK	123	
QY	129	LTVLGQPKAAPS	VTLFPPSS	BELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT	188	
DB	124	LTVLGQPKAAPS	VTLFPPSS	BELOANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT	183	
QY	189	TPSKOSNNKYA	ASSVLSLT	TPQWKSHRSYSCQVTHEGSTVKTVPTECS	238	
DB	184	TPSKOSNNKYA	ASSVLSLT	TPQWKSHRSYSCQVTHEGSTVKTVPTECS	233	

RESULT 2

S25757  
Ig lambda chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25757  
R:Combiato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin 1  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25757  
A:Status: preliminary; translation not shown

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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:53:14 ; Search time 144.896 Seconds  
(without alignments)  
635.274 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KUTMGVPTQVLGLLMLTD.....CQVTHGSEVKTVAFTCS 238

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	238	8	ADRI2638 Mammalian
2	1089	87.6	235	2	Aaw88465 Monoclonal
3	1070.5	86.1	236	2	Aaw63764 Macaque p
4	1070.5	86.1	236	5	Aaui1645 Protein s
5	1070.5	86.1	236	6	Aaui1645 Protein s
6	1067.5	85.9	236	6	Aaui1821 Primatise
7	1067	85.8	233	8	Aaui1821 Human sof
8	1067	85.8	268	5	Abp62895 Human pol
9	1063	85.5	236	4	Abg23083 Novel hum
10	1043	83.9	235	4	Aab36214 Human inm
11	1042	83.8	248	4	Abg26352 Novel hum
12	1027.5	82.7	614	5	Abb06275 Plasmid s
13	1027	82.6	234	8	Abm84293 Human dia
14	1021	82.1	234	8	Abm84291 Human dia
15	1019.5	82.0	235	8	Abm85086 Human dia
16	1018.5	81.9	235	8	Abm85086 Human dia
17	1011	81.3	214	6	Abro1470 Human ant
18	1010	81.3	236	4	Aab36209 Human inm
19	1007.5	81.1	213	6	Abro1475 Human ant
20	1007	81.0	214	6	Abro1467 Human ant
21	1004.5	80.8	213	6	Abro1468 Human ant
22	996	80.1	217	2	Aaw40533 Antibody
23	995	80.0	217	2	Aar42163 Anti-HIV-
24	986.5	79.4	234	6	Abg73422 Human Igg
25	981.5	79.0	234	7	Aae39158 Igg3 anti

26	977	78.6	250	4	ABG19301	Novel hum
27	970	78.0	221	5	ABP52959	Human lun
28	965	77.6	224	8	ABM84279	Human dia
29	964.5	77.6	235	8	ABM84295	Human dia
30	963.5	77.5	235	8	ABM85070	Human dia
31	963.5	77.5	242	6	ABU08021	Monoclonal
32	963.5	77.5	242	7	ADP65786	Human ant
33	963.5	77.5	242	8	ADJ92521	Human ant
34	963	77.5	234	8	ABM85085	Human dia
35	960	77.2	234	8	ABM85071	Human dia
36	959.5	77.2	235	8	ABM84294	Human dia
37	948.5	76.3	249	4	ABG12886	Novel hum
38	944.5	76.0	235	4	AAG64474	Human typ
39	941.5	75.7	251	4	ABG19291	Novel hum
40	940.5	75.7	235	2	AAR31024	Antibody
41	939.5	75.6	234	2	AAR31024	Antibody
42	939.5	75.6	234	2	AAR31024	Antibody
43	939.5	75.6	234	5	AAU11538	Protein s
44	939.5	75.6	234	6	AAE37359	Monkey 7C
45	938.5	75.5	235	4	AAG64476	Human typ

## ALIGNMENTS

RESULT 1  
ADRI2638  
ID ADRI2638 standard; protein; 238 AA.

XX AC ADR12638;  
XX AC ADR12638;  
XX 04-NOV-2004 (first entry)

XX Mammalian anti-Dengue virus antibody light chain.

XX virucide; gene therapy; Dengue virus; antibody; diagnosis; heavy chain.

XX Homo sapiens.

XX WO2004067567-A2.

XX 12-AUG-2004.

XX 30-JAN-2004; 2004WO-EP000896.

XX 31-JAN-2003; 2003US-0443924P.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS PHARMA GMBH.

XX (SRI ) SCRIPPS RES INST.

XX Burton DR, Parren PWI, Yee S;

XX WPI; 2004-594168/57.

XX N-PSDB; ADR12636.

XX New isolated mammalian anti-Dengue virus antibody useful for diagnosing, preventing or treating Dengue virus infection and its associated diseases.

XX Claim 1; SEQ ID NO 4; 111pp; English.

XX The invention relates to an isolated mammalian anti-Dengue virus antibody. The composition, methods and device are useful for diagnosing, preventing or treating Dengue virus infection and its associated diseases. This sequence corresponds to the anti-Dengue virus antibody light chain.

XX Sequence 238 AA;

Query Match 100.0%; Score 1243; DB 8; Length 238;

Best Local Similarity 100.0%; Pred. No. 9.2e-72;

Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;